Using asreml and asremlPlus for the Ladybird example from Welham et al. (2014)

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Introduction

This vignette shows how to use `asremlPlus` (Brien, 2022a), and `dae` (Brien, 2021b), for exploring and presenting predictions from a linear mixed model analysis, the predictions having been produced using `asreml` (Butler et al., 2020). Here, `asremlPlus`, `dae` and `asreml` are packages for the `R` Statistical Computing environment (R Core Team, 2022).

The context is a three-factor factorial experiment on ladybirds (Welham et al., 2014, Example 8.2) that aims to answer the question "Will ladybirds transfer fungus to aphids on plants?" The experiment consists of 2 runs of 36 containers, each with a plant and aphids. There are three factors that results in 12 treatments: Host plant (beans, trefoil), infected Cadavers (5, 10, 20), Ladybird (-, +). Ther are randomized to the containers within a run so that each is replicated 3 times within a run. The respose to be analysed is the logit of the proportion of live aphids that were infected.

Initialize

```
library(knitr)
opts_chunk$set("tidy" = FALSE, comment = NA)
suppressMessages(library(asreml))
```

```
## Offline License checked out Sun Nov 13 08:57:04 2022
```

```
packageVersion("asreml")
```

```
## [1] '4.1.0.176'
```

```
suppressMessages(library(asremlPlus))
packageVersion("asremlPlus")
```

```
## [1] '4.3.39'
```

```
suppressMessages(library("dae"))
packageVersion("dae")
```

```
## [1] '3.2.13'
```

```
options(width = 95, show.signif.stars = FALSE)
```

Get data available in asremlPlus

```
data("Ladybird.dat")
```

Do an ANOVA of logits

```
Ladybird.aov <- aov(logitP ~ Host*Cadavers*Ladybird + Error(Run/Plant),
                     data=Ladybird.dat)
summary(Ladybird.aov)
```

```
Error: Run
          Df  Sum Sq Mean Sq F value Pr(>F)
Residuals  1 0.06766 0.06766

Error: Run:Plant
                      Df Sum Sq Mean Sq F value   Pr(>F)
Host                   1 13.599  13.599  59.172 1.82e-10
Cadavers               2 17.027   8.514  37.044 3.78e-11
Ladybird               1 11.091  11.091  48.257 3.33e-09
Host:Cadavers          2  0.308   0.154   0.670   0.5158
Host:Ladybird          1  0.228   0.228   0.992   0.3234
Cadavers:Ladybird      2  1.735   0.867   3.774   0.0287
Host:Cadavers:Ladybird 2  0.200   0.100   0.435   0.6493
Residuals             59 13.560   0.230
```

The anova table gives the F-tests for the three-factor effects and interactions. Note the `Residuals Mean Sq` value for `Run:Plant` of 0.230. Also, it is clear that the Run component is negative, given that the `Residuals Mean Sq` value for `Run` is less than that for `Run:Plant`; it is $(0.06766 - 0.230) / 36$. From the table it is seen that the only significant interaction is Cadavers:Ladybird and that the Host main effect is significant.

Use asreml to analyse the logits

Mixed model analysis of logits

```
m <- asreml(logitP ~ Host*Cadavers*Ladybird,
            random = ~ Run,
            residual = ~ Run:Plant,
            data = Ladybird.dat)
```

```
Model fitted using the gamma parameterization.
ASReml 4.1.0 Sun Nov 13 08:57:04 2022
        LogLik       Sigma2    DF      wall    cpu
  1    3.07130     0.226239    60 08:57:04    0.0 (1 restrained)
  2    3.64260     0.226912    60 08:57:04    0.0 (1 restrained)
  3    3.71250     0.227106    60 08:57:04    0.0 (1 restrained)
  4    3.71721     0.227121    60 08:57:04    0.0 (1 restrained)
  5    3.71751     0.227122    60 08:57:04    0.0 (1 restrained)
```

Warning in asreml(logitP ~ Host * Cadavers * Ladybird, random = ~Run, residual = ~Run:Plant, :
Some components changed by more than 1% on the last iteration.

```
summary(m)$varcomp
```

```
              component  std.error  z.ratio bound  %ch
Run        2.298309e-08         NA       NA     B 93.7
Run:Plant!R 2.271216e-01 0.04156985 5.463612     P  0.0
```

As expected the Run component is bound (`B`) at approximately zero. This results in a change in the estimate of the residual variance to 0.227. To allow for a negative estimate we will unconstrain the Run component.

As Littell et al. (2006, p.150) say

> if you do not set the negative variance component estimate to zero, but allow it to remain negative, you get better control over Type I error and, for cases of negative wholeplot error variance estimates, greater power. Therefore, this is the recommended procedure.

Unconstrain Reps to make the analysis equivalent to ANOVA

```
m <- setvarianceterms(m$call, terms = "Run", bounds = "U")
```

```
Model fitted using the gamma parameterization.
ASReml 4.1.0 Sun Nov 13 08:57:04 2022
          LogLik       Sigma2     DF     wall     cpu
  1      3.07130     0.226239     60 08:57:04     0.0 (1 restrained)
  2      3.64260     0.226912     60 08:57:04     0.0 (1 restrained)
  3      3.80283     0.227454     60 08:57:04     0.0 (1 restrained)
  4      3.83949     0.233418     60 08:57:04     0.0
  5      3.95568     0.230971     60 08:57:04     0.0
  6      3.97333     0.230035     60 08:57:04     0.0
  7      3.97405     0.229835     60 08:57:04     0.0
```

```
summary(m)$varcomp
```

```
              component    std.error   z.ratio bound %ch
Run         -0.004504789 0.002896281 -1.555370     U 0.1
Run:Plant!R  0.229834648 0.042316936  5.431269     P 0.0
```

Now the `Run` component is negative and the `Run:Plant` variance estimate is now equal to that for the Residuals Mean Sq for `Run:Plant` from the anova table.

Set up an asrtests object

```
current.asrt <- as.asrtests(m)
```

Calculating denominator DF

```
print(current.asrt, which = "pseudoanova")
```

```
####  Pseudo-anova table for fixed terms
```

```
Wald tests for fixed effects.
Response: logitP
```

	Df	denDF	F.inc	Pr
(Intercept)	1	1	1550.00	0.0162
Host	1	59	59.17	0.0000
Cadavers	2	59	37.04	0.0000
Ladybird	1	59	48.26	0.0000
Host:Cadavers	2	59	0.67	0.5158
Host:Ladybird	1	59	0.99	0.3234
Cadavers:Ladybird	2	59	3.77	0.0287
Host:Cadavers:Ladybird	2	59	0.44	0.6493

The `asrtests` object contains a `wald.tab` component which can be printed by specifying that the `pseudoanova` is printed. The F-values for the fixed terms in this table are the same as those in the anova table.

Obtain the marginality matrix for the fixed terms

The `pstructure` function from the `dae` package (Brien, 2021) produce the marginality matrix for a formula as a side effect and we take advantage of that to obtain the matrix required here.

```
Ladybird.pstr <- pstructure(formula = ~ Host*Cadavers*Ladybird,
                            data = Ladybird.dat)
HCL.marg <- marginality(Ladybird.pstr)
print(HCL.marg)
```

```
                      Host Cadavers Host:Cadavers Ladybird Host:Ladybird Cadavers:Ladybird
Host                     1        0             1        0             1                 0
Cadavers                 0        1             1        0             0                 1
Host:Cadavers            0        0             1        0             0                 0
Ladybird                 0        0             0        1             1                 1
Host:Ladybird            0        0             0        0             1                 0
Cadavers:Ladybird        0        0             0        0             0                 1
Host:Cadavers:Ladybird   0        0             0        0             0                 0
                      Host:Cadavers:Ladybird
Host                                       1
Cadavers                                   1
Host:Cadavers                              1
Ladybird                                   1
Host:Ladybird                              1
Cadavers:Ladybird                          1
Host:Cadavers:Ladybird                     1
```

This marginality matrix is interpreted by taking a row term and noting that it is marginal to any column term with a one in this row.

Choose marginality-compliant model

```
chosen <- chooseModel(current.asrt, terms.marginality = HCL.marg)
```

```
Calculating denominator DF


####  Sequence of model investigations

(If a row has NA for p but not denDF, DF and denDF relate to fixed and variance parameter numbers)

                  terms DF denDF      p AIC BIC         action
1 Host:Cadavers:Ladybird  2    59 0.6493  NA  NA Nonsignificant
Calculating denominator DF


####  Sequence of model investigations

(If a row has NA for p but not denDF, DF and denDF relate to fixed and variance parameter numbers)

                  terms DF denDF      p AIC BIC         action
1 Host:Cadavers:Ladybird  2    59 0.6493  NA  NA Nonsignificant
2     Cadavers:Ladybird  2    59 0.0287  NA  NA    Significant
```

```
Calculating denominator DF


#### Sequence of model investigations

(If a row has NA for p but not denDF, DF and denDF relate to fixed and variance parameter numbers)

                   terms DF denDF      p AIC BIC         action
1 Host:Cadavers:Ladybird  2    59 0.6493  NA  NA Nonsignificant
2     Cadavers:Ladybird  2    59 0.0287  NA  NA    Significant
3         Host:Ladybird  1    59 0.3234  NA  NA Nonsignificant
Calculating denominator DF


#### Sequence of model investigations

(If a row has NA for p but not denDF, DF and denDF relate to fixed and variance parameter numbers)

                   terms DF denDF      p AIC BIC         action
1 Host:Cadavers:Ladybird  2    59 0.6493  NA  NA Nonsignificant
2     Cadavers:Ladybird  2    59 0.0287  NA  NA    Significant
3         Host:Ladybird  1    59 0.3234  NA  NA Nonsignificant
4         Host:Cadavers  2    59 0.5158  NA  NA Nonsignificant
Calculating denominator DF


#### Sequence of model investigations

(If a row has NA for p but not denDF, DF and denDF relate to fixed and variance parameter numbers)

                   terms DF denDF      p AIC BIC         action
1 Host:Cadavers:Ladybird  2    59 0.6493  NA  NA Nonsignificant
2     Cadavers:Ladybird  2    59 0.0287  NA  NA    Significant
3         Host:Ladybird  1    59 0.3234  NA  NA Nonsignificant
4         Host:Cadavers  2    59 0.5158  NA  NA Nonsignificant
5                 Host  1    59 0.0000  NA  NA    Significant
```

```r
current.asrt <- chosen$asrtests.obj
print(current.asrt, which = "test", omit.columns = c("AIC", "BIC"))
```

```
#### Sequence of model investigations

                   terms DF denDF      p         action
1 Host:Cadavers:Ladybird  2    59 0.6493 Nonsignificant
2     Cadavers:Ladybird  2    59 0.0287    Significant
3         Host:Ladybird  1    59 0.3234 Nonsignificant
4         Host:Cadavers  2    59 0.5158 Nonsignificant
5                 Host  1    59 0.0000    Significant
```

```r
(chosen$sig.terms)
```

```
[[1]]
[1] "Cadavers:Ladybird"
```

```
[[2]]
[1] "Host"
```

The `chooseModel` function produces a list with components `sig.terms`, a list with the terms in the marginality-compliant model, and `asrtests.obj`, the `asrtests` object resulting from the model selection. In particular, the `asrtests` object contains a `test.summary` that details the tests performed in choosing the model; the `AIC` and `BIC` columns are omitted from `test.summary` because their incluson has not been requested. Note that `chooseModel` does not test the main effects for Cadavers or Ladybird, because these are marginal to the significant two-factor interaction Cadavers:Ladybird.

Form formula for selected model

```
chosen.mod <- paste(unlist(chosen$sig.terms), collapse = " + ")
(chosen.mod <- as.formula(paste("~", chosen.mod)))

~Cadavers:Ladybird + Host
```

Obtain predictions under the chosen model and form an alldiffs object

```
diffs <- predictPlus(current.asrt$asreml.obj,
                     classify = "Host:Ladybird:Cadavers",
                     linear.transformation = ~Cadavers:Ladybird + Host,
                     wald.tab = current.asrt$wald.tab,
                     error.intervals = "halfLeast",
                     LSDtype = "factor.combination", LSDby = "Host",
                     tables = "predictions")
```

```
#### Predictions for logitP transform(s) from Host:Ladybird:Cadavers


Notes:
The original predictions, obtained as described below, have
been linearly transformed to form estimated marginal means.
- The predictions are obtained by averaging across the hypertable
  calculated from model terms constructed solely from factors in
  the averaging and classify sets.
- Use 'average' to move ignored factors into the averaging set.
- The ignored set: Run
```

	Host	Ladybird	Cadavers	predicted.value	standard.error	upper.halfLeastSignificant.limit
1	bean	–	5	-1.6038338	0.1417454	-1.4080222
2	bean	–	10	-1.1454308	0.1417454	-0.9496192
3	bean	–	20	-0.7448097	0.1417454	-0.5489981
4	bean	+	5	-1.0195475	0.1417454	-0.8237359
5	bean	+	10	-0.5983440	0.1417454	-0.4025323
6	bean	+	20	0.4786704	0.1417454	0.6744820
7	trefoil	–	5	-2.4730339	0.1417454	-2.2772223
8	trefoil	–	10	-2.0146309	0.1417454	-1.8188193
9	trefoil	–	20	-1.6140098	0.1417454	-1.4181982
10	trefoil	+	5	-1.8887476	0.1417454	-1.6929360
11	trefoil	+	10	-1.4675441	0.1417454	-1.2717325
12	trefoil	+	20	-0.3905297	0.1417454	-0.1947181

```
    lower.halfLeastSignificant.limit est.status
1                         -1.7996454  Estimable
2                         -1.3412425  Estimable
3                         -0.9406214  Estimable
4                         -1.2153592  Estimable
5                         -0.7941556  Estimable
6                          0.2828588  Estimable
7                         -2.6688455  Estimable
8                         -2.2104426  Estimable
9                         -1.8098215  Estimable
10                        -2.0845593  Estimable
11                        -1.6633557  Estimable
12                        -0.5863414  Estimable


LSD values

minimum LSD =  0.3916233 0.3916233

mean LSD =  0.3916233 0.3916233

maximum LSD =  0.3916233 0.3916233

(sed range / mean sed =  5.67e-16 7.09e-16 )
```

Setting the `terms` argument to `Host:Ladybird:Cadavers` requests predictions for all combinations of the three factors and the `linear.transformation` argument is used to obtain estimated marginal means (emm) that conform to the chosen model. The `wald.tab` is supplied so that it can be used to get the degrees of freedom for the *t*-value to be used in calculating the LSD; the degrees of freedom ot the source for the `terms` argument will be used. The `error.intervals` argument has been set to `"halfLeast"`, the `LSDtype` argument to `"factor.combination"` and the `LSDby` argument to `"Host"` so that the average LSD will be calculated for each Host. This necessary because, under the chosen model, the LSDs differ between Hosts. It results in `lower.halfLeastSignificant.limit` and `upper.halfLeastSignificant.limit` being added to the `predictions` component of the `alldiffs` object.

Or, caclulate predictions to check first and then transform to conform to chosen model

```
diffs.full <- predictPlus(current.asrt$asreml.obj,
                    classify = "Host:Ladybird:Cadavers",
                    wald.tab = current.asrt$wald.tab,
                    tables = "none", Vmatrix = TRUE)

diffs <- linTransform(diffs.full, linear.transformation = ~Cadavers:Ladybird + Host,
                    wald.tab = current.asrt$wald.tab,
                    error.intervals = "halfLeast",
                    LSDtype = "factor.combination", LSDby = "Host",
                    tables = "predictions")
```

Predictions for logitP transform(s) from Host:Ladybird:Cadavers

```
Notes:
```

The original predictions, obtained as described below, have
been linearly transformed to form estimated marginal means.
- The predictions are obtained by averaging across the hypertable
  calculated from model terms constructed solely from factors in
  the averaging and classify sets.
- Use 'average' to move ignored factors into the averaging set.
- The ignored set: Run

```
      Host Ladybird Cadavers predicted.value standard.error upper.halfLeastSignificant.limit
1      bean        -        5      -1.6038338      0.1417454                     -1.4080222
2      bean        -       10      -1.1454308      0.1417454                     -0.9496192
3      bean        -       20      -0.7448097      0.1417454                     -0.5489981
4      bean        +        5      -1.0195475      0.1417454                     -0.8237359
5      bean        +       10      -0.5983440      0.1417454                     -0.4025323
6      bean        +       20       0.4786704      0.1417454                      0.6744820
7   trefoil        -        5      -2.4730339      0.1417454                     -2.2772223
8   trefoil        -       10      -2.0146309      0.1417454                     -1.8188193
9   trefoil        -       20      -1.6140098      0.1417454                     -1.4181982
10  trefoil        +        5      -1.8887476      0.1417454                     -1.6929360
11  trefoil        +       10      -1.4675441      0.1417454                     -1.2717325
12  trefoil        +       20      -0.3905297      0.1417454                     -0.1947181
    lower.halfLeastSignificant.limit est.status
1                         -1.7996454  Estimable
2                         -1.3412425  Estimable
3                         -0.9406214  Estimable
4                         -1.2153592  Estimable
5                         -0.7941556  Estimable
6                          0.2828588  Estimable
7                         -2.6688455  Estimable
8                         -2.2104426  Estimable
9                         -1.8098215  Estimable
10                        -2.0845593  Estimable
11                        -1.6633557  Estimable
12                        -0.5863414  Estimable
```

LSD values

minimum LSD = 0.3916233 0.3916233

mean LSD = 0.3916233 0.3916233

maximum LSD = 0.3916233 0.3916233

(sed range / mean sed = 5.67e-16 7.09e-16)

Plot the predictions

```
plotPredictions(diffs$predictions, y ="predicted.value",
                y.title = "logit(P) estimated marginal means",
                classify = "Host:Ladybird:Cadavers",
                error.intervals = "halfLeast",
                ggplotFuncs = list(facet_grid(Ladybird ~ Host,
                                              labeller = label_both)))
```
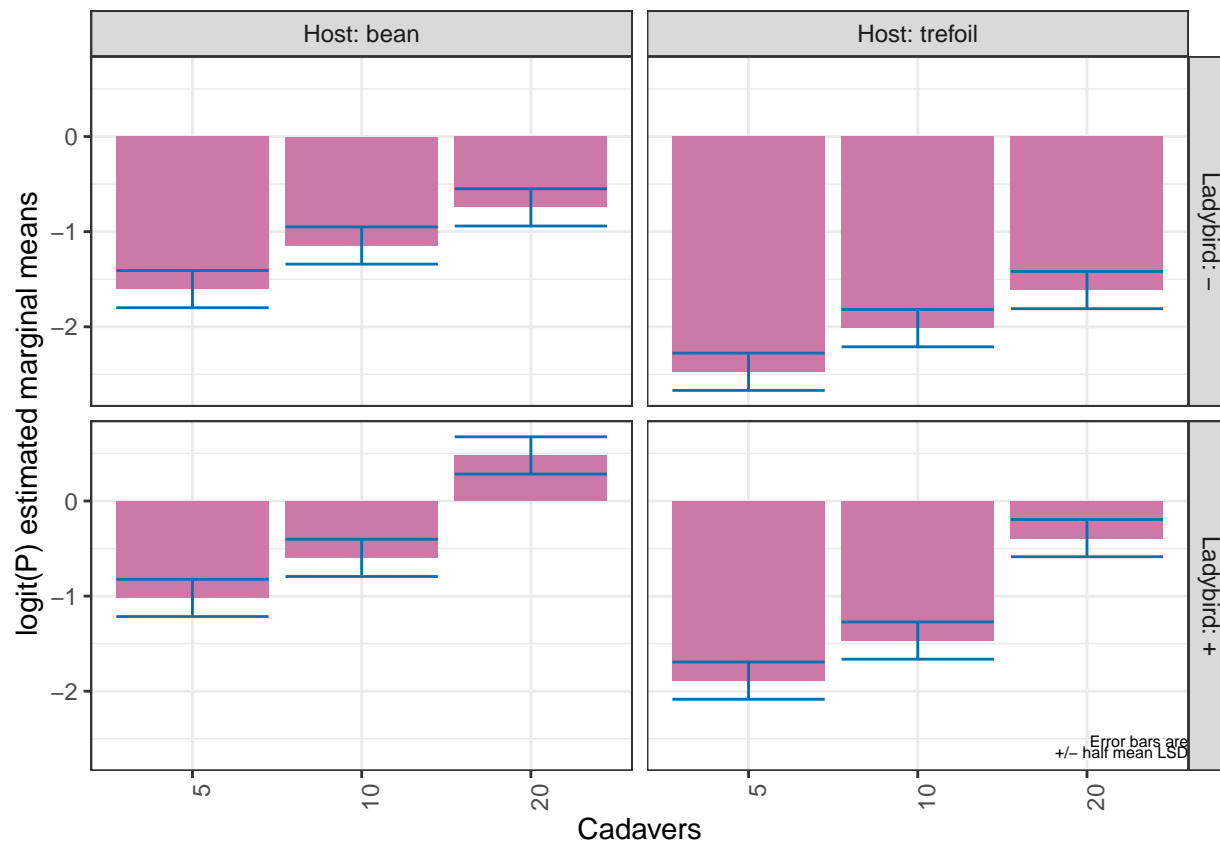
The function `plotPredictions` uses `ggplot` to produce the plot and the `ggplotFuncs` argument allows the addition of `ggplot` functions to modify the plot. In this case, the `facet.grid` function is respecified to include `prepender` functions that modify the labels of the facets to include the factor names. Note the the error bars in the plots are of $\pm 0.5 LSD$ so that pairs of prediction with nonoverlapping bars are significantly different (Snee, 1981).

Get and plot the predictions with a single function call

The `predictPresent` function combines the functionality of `predictPlus` and `plotPredictions`, as demonstrated now. Also, the use of `plotPvalues` to plot the pairwise p-values is displayed. The `predictPresent` function has the capability of producing `alldiffs` objects for multiple `terms` and these are stored in a list each of which is named for the term whose `alldiffs` object it stores. Thus, the term has to be specified in referencing components of `diffs`.

```
titl <- "logit(P) estimated marginal means"
names(titl) <- "logitP"
diffs <- predictPresent(current.asrt$asreml.obj,
                        terms = "Host:Ladybird:Cadavers",
                        linear.transformation = ~Cadavers:Ladybird + Host,
                        titles = titl,
                        wald.tab = current.asrt$wald.tab,
                        error.intervals = "halfLeast",
                        LSDtype = "factor.combination", LSDby = "Host",
                        tables = "none",
                        ggplotFuncs = list(facet_grid(Ladybird ~ Host,
                                                      labeller = label_both)))
```

Error bars are +/− half mean LSD
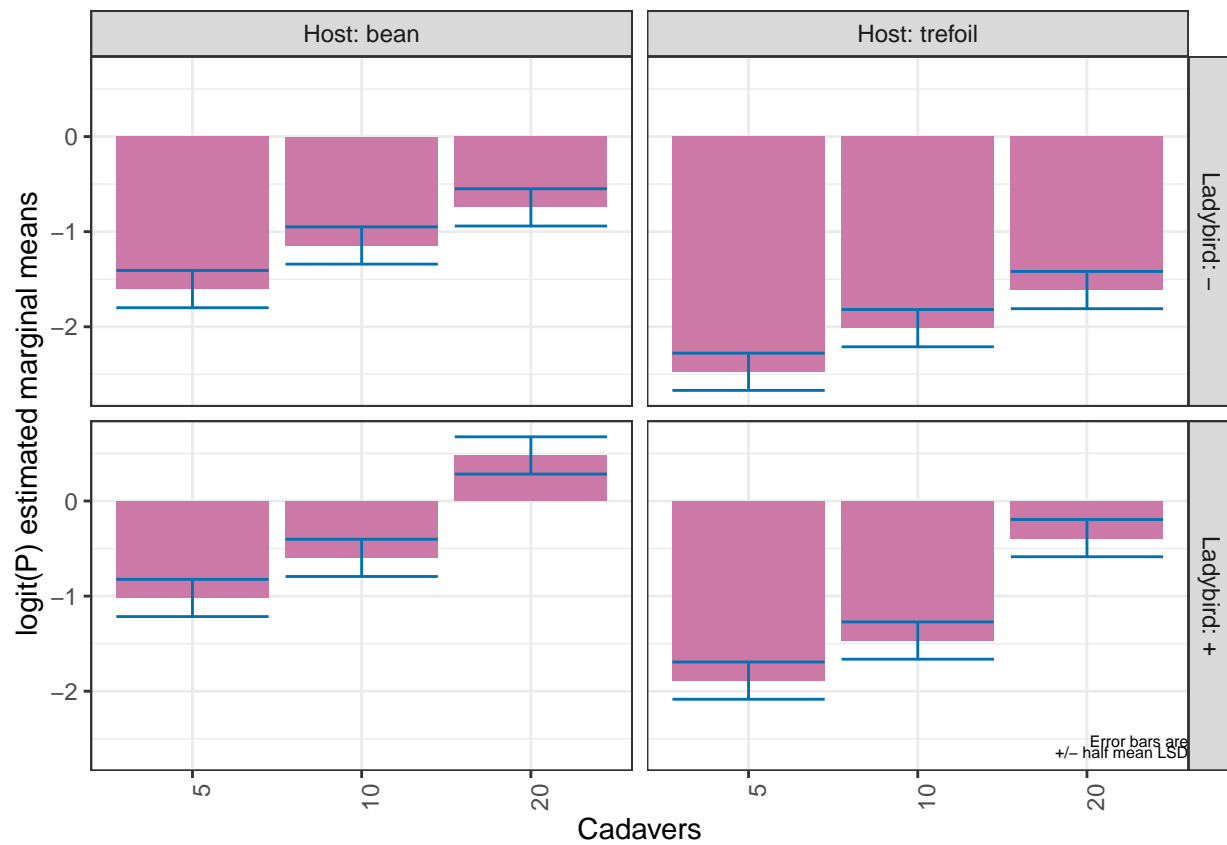
```
plotPvalues(diffs$Host.Ladybird.Cadavers, factors.per.grid = 1, show.sig = TRUE)
```
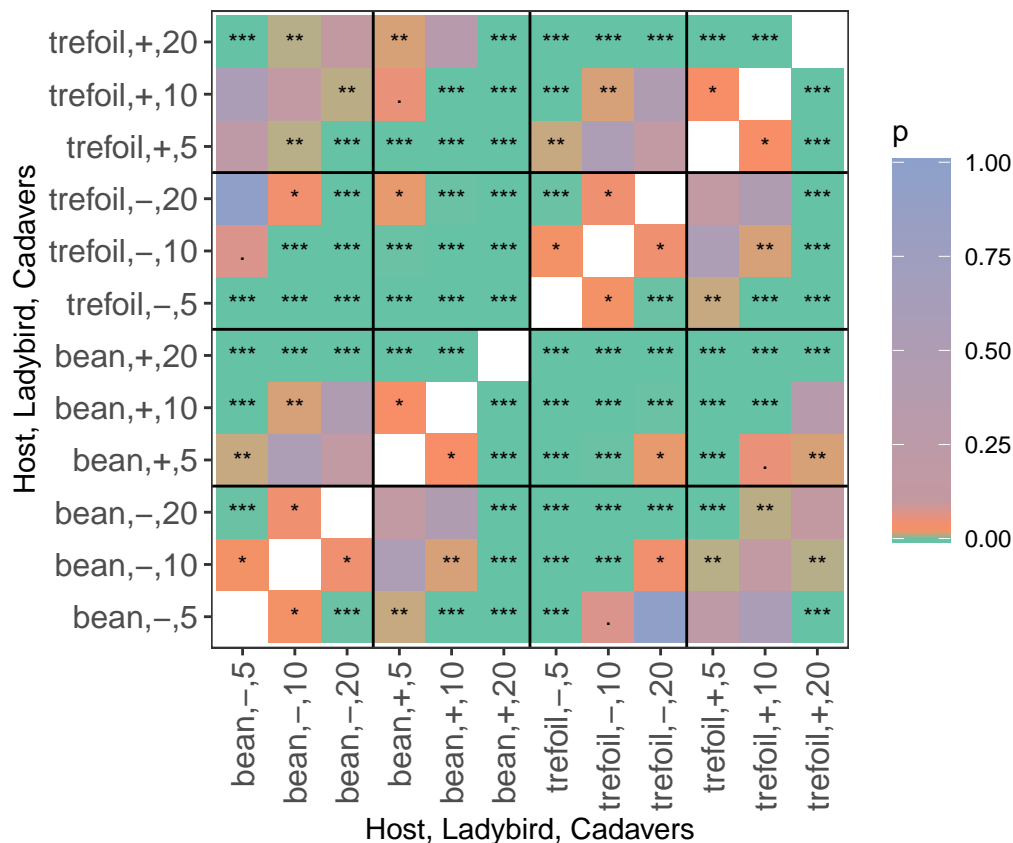
```
options(width = 90)
diffs$Host.Ladybird.Cadavers$differences
```

```
                bean,-,5   bean,-,10  bean,-,20   bean,+,5   bean,+,10  bean,+,20
bean,-,5       0.00000000 -0.4584030 -0.8590241 -0.5842863 -1.0054898 -2.0825042
bean,-,10      0.45840297  0.0000000 -0.4006211 -0.1258833 -0.5470869 -1.6241012
bean,-,20      0.85902408  0.4006211  0.0000000  0.2747378 -0.1464657 -1.2234801
bean,+,5       0.58428627  0.1258833 -0.2747378  0.0000000 -0.4212036 -1.4982179
bean,+,10      1.00548982  0.5470869  0.1464657  0.4212036  0.0000000 -1.0770144
bean,+,20      2.08250420  1.6241012  1.2234801  1.4982179  1.0770144  0.0000000
trefoil,-,5   -0.86920012 -1.3276031 -1.7282242 -1.4534864 -1.8746899 -2.9517043
trefoil,-,10  -0.41079715 -0.8692001 -1.2698212 -0.9950834 -1.4162870 -2.4933014
trefoil,-,20  -0.01017604 -0.4685790 -0.8692001 -0.5944623 -1.0156659 -2.0926802
trefoil,+,5   -0.28491385 -0.7433168 -1.1439379 -0.8692001 -1.2904037 -2.3674180
trefoil,+,10   0.13628970 -0.3221133 -0.7227344 -0.4479966 -0.8692001 -1.9462145
trefoil,+,20   1.21330408  0.7549011  0.3542800  0.6290178  0.2078143 -0.8692001
                trefoil,-,5 trefoil,-,10 trefoil,-,20 trefoil,+,5 trefoil,+,10 trefoil,+,20
bean,-,5          0.8692001    0.4107972   0.01017604   0.2849139   -0.1362897   -1.2133041
bean,-,10         1.3276031    0.8692001   0.46857901   0.7433168    0.3221133   -0.7549011
bean,-,20         1.7282242    1.2698212   0.86920012   1.1439379    0.7227344   -0.3542800
bean,+,5          1.4534864    0.9950834   0.59446231   0.8692001    0.4479966   -0.6290178
bean,+,10         1.8746899    1.4162870   1.01566586   1.2904037    0.8692001   -0.2078143
bean,+,20         2.9517043    2.4933014   2.09268024   2.3674180    1.9462145    0.8692001
trefoil,-,5       0.0000000   -0.4584030  -0.85902408  -0.5842863   -1.0054898   -2.0825042
trefoil,-,10      0.4584030    0.0000000  -0.40062111  -0.1258833   -0.5470869   -1.6241012
trefoil,-,20      0.8590241    0.4006211   0.00000000   0.2747378   -0.1464657   -1.2234801
```

```
trefoil,+,5     0.5842863    0.1258833  -0.27473781    0.0000000   -0.4212036   -1.4982179
trefoil,+,10    1.0054898    0.5470869   0.14646574    0.4212036    0.0000000   -1.0770144
trefoil,+,20    2.0825042    1.6241012   1.22348012    1.4982179    1.0770144    0.0000000
```

```
options(width = 90)
print(diffs$Host.Ladybird.Cadavers$sed)
```

```
              bean,-,5 bean,-,10 bean,-,20  bean,+,5 bean,+,10 bean,+,20 trefoil,-,5
bean,-,5            NA 0.1957142 0.1957142 0.1957142 0.1957142 0.1957142   0.1129957
bean,-,10    0.1957142        NA 0.1957142 0.1957142 0.1957142 0.1957142   0.2259913
bean,-,20    0.1957142 0.1957142        NA 0.1957142 0.1957142 0.1957142   0.2259913
bean,+,5     0.1957142 0.1957142 0.1957142        NA 0.1957142 0.1957142   0.2259913
bean,+,10    0.1957142 0.1957142 0.1957142 0.1957142        NA 0.1957142   0.2259913
bean,+,20    0.1957142 0.1957142 0.1957142 0.1957142 0.1957142        NA   0.2259913
trefoil,-,5  0.1129957 0.2259913 0.2259913 0.2259913 0.2259913 0.2259913          NA
trefoil,-,10 0.2259913 0.1129957 0.2259913 0.2259913 0.2259913 0.2259913   0.1957142
trefoil,-,20 0.2259913 0.2259913 0.1129957 0.2259913 0.2259913 0.2259913   0.1957142
trefoil,+,5  0.2259913 0.2259913 0.2259913 0.1129957 0.2259913 0.2259913   0.1957142
trefoil,+,10 0.2259913 0.2259913 0.2259913 0.2259913 0.1129957 0.2259913   0.1957142
trefoil,+,20 0.2259913 0.2259913 0.2259913 0.2259913 0.2259913 0.1129957   0.1957142
             trefoil,-,10 trefoil,-,20 trefoil,+,5 trefoil,+,10 trefoil,+,20
bean,-,5        0.2259913    0.2259913   0.2259913    0.2259913    0.2259913
bean,-,10       0.1129957    0.2259913   0.2259913    0.2259913    0.2259913
bean,-,20       0.2259913    0.1129957   0.2259913    0.2259913    0.2259913
bean,+,5        0.2259913    0.2259913   0.1129957    0.2259913    0.2259913
bean,+,10       0.2259913    0.2259913   0.2259913    0.1129957    0.2259913
bean,+,20       0.2259913    0.2259913   0.2259913    0.2259913    0.1129957
trefoil,-,5     0.1957142    0.1957142   0.1957142    0.1957142    0.1957142
trefoil,-,10           NA    0.1957142   0.1957142    0.1957142    0.1957142
trefoil,-,20    0.1957142           NA   0.1957142    0.1957142    0.1957142
trefoil,+,5     0.1957142    0.1957142          NA    0.1957142    0.1957142
trefoil,+,10    0.1957142    0.1957142   0.1957142           NA    0.1957142
trefoil,+,20    0.1957142    0.1957142   0.1957142    0.1957142           NA
```

Perform the analysis with just selected model fitted

The model with nonsignificant fixed terms dropped is obtained in order to compare it with the fit when they are retained and the etimated marginal means for the chosen model are obtained.

```
ns.terms <- current.asrt$test.summary$terms[current.asrt$test.summary$action == "Nonsignificant"]
red.asrt <- changeTerms(current.asrt, dropFixed = paste(ns.terms, collapse = "+"))
```

```
Calculating denominator DF
Calculating denominator DF
```

```
summary(red.asrt$asreml.obj)$varcomp
```

```
              component     std.error   z.ratio bound %ch
Run        -0.004327123 0.002802858 -1.543825     U 0.8
Run:Plant!R 0.223431515 0.039503521  5.655990     P 0.0
```

```
print(red.asrt, which = "pseudoanova")
```

```
####  Pseudo-anova table for fixed terms
```

12

```
Wald tests for fixed effects.
Response: logitP


                 Df denDF   F.inc      Pr
(Intercept)       1     1 1550.00 0.0162
Host              1    64   60.88 0.0000
Cadavers          2    64   38.12 0.0000
Ladybird          1    64   49.65 0.0000
Cadavers:Ladybird 2    64    3.88 0.0256
```

```r
diffs.red <- predictPlus(red.asrt$asreml.obj,
                    classify = "Host:Ladybird:Cadavers",
                    wald.tab = current.asrt$wald.tab,
                    error.intervals = "halfLeast",
                    LSDtype = "factor.combination", LSDby = "Host",
                    tables = "predictions")
```

Predictions for logitP from Host:Ladybird:Cadavers

Notes:
- The predictions are obtained by averaging across the hypertable
  calculated from model terms constructed solely from factors in
  the averaging and classify sets.
- Use 'average' to move ignored factors into the averaging set.
- The ignored set: Run

```
     Host Ladybird Cadavers predicted.value standard.error
1     bean        -        5      -1.6038338      0.1398332
2     bean        -       10      -1.1454308      0.1398332
3     bean        -       20      -0.7448097      0.1398332
4     bean        +        5      -1.0195475      0.1398332
5     bean        +       10      -0.5983440      0.1398332
6     bean        +       20       0.4786704      0.1398332
7   trefoil        -        5      -2.4730339      0.1398332
8   trefoil        -       10      -2.0146309      0.1398332
9   trefoil        -       20      -1.6140098      0.1398332
10  trefoil        +        5      -1.8887476      0.1398332
11  trefoil        +       10      -1.4675441      0.1398332
12  trefoil        +       20      -0.3905297      0.1398332
   upper.halfLeastSignificant.limit lower.halfLeastSignificant.limit est.status
1                        -1.4107942                       -1.7968734  Estimable
2                        -0.9523913                       -1.3384704  Estimable
3                        -0.5517702                       -0.9378493  Estimable
4                        -0.8265080                       -1.2125871  Estimable
5                        -0.4053044                       -0.7913835  Estimable
6                         0.6717100                        0.2856308  Estimable
7                        -2.2799944                       -2.6660735  Estimable
8                        -1.8215914                       -2.2076705  Estimable
9                        -1.4209703                       -1.8070494  Estimable
10                       -1.6957081                       -2.0817872  Estimable
11                       -1.2745045                       -1.6605837  Estimable
```

```
12                      -0.1974902                          -0.5835693  Estimable


LSD values

minimum LSD =  0.3860791 0.3860791

mean LSD =  0.3860791 0.3860791

maximum LSD =  0.3860791 0.3860791

(sed range / mean sed =  2.44e-15 2.3e-15 )
```

```r
options(width = 90)
print(diffs.red$sed)
```

```
            bean,-,5 bean,-,10 bean,-,20  bean,+,5 bean,+,10 bean,+,20 trefoil,-,5
bean,-,5          NA 0.1929435 0.1929435 0.1929435 0.1929435 0.1929435   0.1113960
bean,-,10  0.1929435        NA 0.1929435 0.1929435 0.1929435 0.1929435   0.2227920
bean,-,20  0.1929435 0.1929435        NA 0.1929435 0.1929435 0.1929435   0.2227920
bean,+,5   0.1929435 0.1929435 0.1929435        NA 0.1929435 0.1929435   0.2227920
bean,+,10  0.1929435 0.1929435 0.1929435 0.1929435        NA 0.1929435   0.2227920
bean,+,20  0.1929435 0.1929435 0.1929435 0.1929435 0.1929435        NA   0.2227920
trefoil,-,5  0.1113960 0.2227920 0.2227920 0.2227920 0.2227920 0.2227920        NA
trefoil,-,10 0.2227920 0.1113960 0.2227920 0.2227920 0.2227920 0.2227920   0.1929435
trefoil,-,20 0.2227920 0.2227920 0.1113960 0.2227920 0.2227920 0.2227920   0.1929435
trefoil,+,5  0.2227920 0.2227920 0.2227920 0.1113960 0.2227920 0.2227920   0.1929435
trefoil,+,10 0.2227920 0.2227920 0.2227920 0.2227920 0.1113960 0.2227920   0.1929435
trefoil,+,20 0.2227920 0.2227920 0.2227920 0.2227920 0.2227920 0.1113960   0.1929435
            trefoil,-,10 trefoil,-,20 trefoil,+,5 trefoil,+,10 trefoil,+,20
bean,-,5       0.2227920    0.2227920   0.2227920    0.2227920    0.2227920
bean,-,10      0.1113960    0.2227920   0.2227920    0.2227920    0.2227920
bean,-,20      0.2227920    0.1113960   0.2227920    0.2227920    0.2227920
bean,+,5       0.2227920    0.2227920   0.1113960    0.2227920    0.2227920
bean,+,10      0.2227920    0.2227920   0.2227920    0.1113960    0.2227920
bean,+,20      0.2227920    0.2227920   0.2227920    0.2227920    0.1113960
trefoil,-,5    0.1929435    0.1929435   0.1929435    0.1929435    0.1929435
trefoil,-,10          NA    0.1929435   0.1929435    0.1929435    0.1929435
trefoil,-,20   0.1929435           NA   0.1929435    0.1929435    0.1929435
trefoil,+,5    0.1929435    0.1929435          NA    0.1929435    0.1929435
trefoil,+,10   0.1929435    0.1929435   0.1929435           NA    0.1929435
trefoil,+,20   0.1929435    0.1929435   0.1929435    0.1929435           NA
```

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